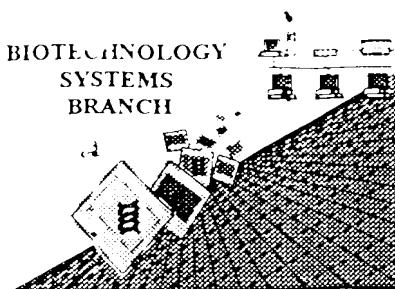


RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/002,292

Source: COPE

Date Processed by STIC: 12/11/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER: 06/04/001

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1. Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
2. Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
3. Misaligned Amino The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead
4. Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
5. Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
6. PatentIn 2.0 A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences
7. Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence (OLD RULES)
 - (2) INFORMATION FOR SEQ ID NO X (insert SEQ ID NO where "X" is shown)
 - (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading)
 - (xi) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown)

This sequence is intentionally skipped

Please also adjust the "(i) NUMBER OF SEQUENCES" response to include the skipped sequences
8. Skipped Sequences Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence (NEW RULES)
 - <210> sequence id number
 - <400> sequence id number
 - 000
9. Use of n's or Xaa's Use of n's and/or Xaa's have been detected in the Sequence Listing. (NEW RULES)
 - Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present
 - In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents
10. Invalid <213> Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or Response scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
11. ✓ Use of <220> Sequence(s) 11-14 missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (See 1.823 of Sequence Rules)
12. PatentIn 2.0 Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, "bug" resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/002,292

DATE: 12/11/2001

TIME: 12:04:32

Input Set : A:\ES.txt

Output Set: N:\CRF3\12112001\I002292.raw

```

3 110> APPLICANT: Ward, Brian
4      Snyder, Leanne
5      Li, Chuan
6      Song, Kemin
7      Oppen, Kristen
8      Uder, Stephanie
9      Hernan, Ron
11 <120> TITLE OF INVENTION: RECOMBINANT DNA PROCESSES USING A dNTP MIXTURE CONTAINING
MODIFIED
12      NUCLEOTIDES
14 <130> FILE REFERENCE: SGM 6938.1
C--> 16 <140> CURRENT APPLICATION NUMBER: US/10/002,292
C--> 16 <141> CURRENT FILING DATE: 2001-11-15
16 <150> PRIOR APPLICATION NUMBER: US 60/325,612
17 <151> PRIOR FILING DATE: 2001-09-28
19 <160> NUMBER OF SEQ ID NOS: 14
21 <170> SOFTWARE: PatentIn version 3.0
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 28
25 <212> TYPE: DNA
26 <213> ORGANISM: Lambda phage
28 <220> FEATURE
29 <221> NAME: FEY misc_feature
30 <222> LOCATION: (1)..(28)
31 <223> OTHER INFORMATION: Primer for Polymerase Chain Reaction (PCR)
34 <400> SEQUENCE: 1
35 gatcgaatgaq ttcgtatccq tacaactg 28
38 <210> SEQ ID NO: 2
39 <211> LENGTH: 28
40 <212> TYPE: DNA
41 <213> ORGANISM: Lambda phage
43 <220> FEATURE
44 <221> NAME: FEY misc_feature
45 <222> LOCATION: (1)..(28)
46 <223> OTHER INFORMATION: Primer for Polymerase Chain Reaction (PCR)
49 <400> SEQUENCE: 2
50 ctaqaattat cgaatcaga cacaacgc 28
53 <210> SEQ ID NO: 3
54 <211> LENGTH: 35
55 <212> TYPE: DNA
56 <213> ORGANISM: Lambda phage
58 <220> FEATURE
59 <221> NAME: FEY misc_feature
60 <222> LOCATION: (1)..(35)
61 <223> OTHER INFORMATION: Primer for Polymerase Chain Reaction (PCR)
64 <400> SEQUENCE: 3
65 gcacgggac cgaatgaattc gtatccgtac aactg 35
68 <210> SEQ ID NO: 4

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RAW SEQUENCE LISTING

PATENT APPLICATION NO. US/10/002,292

DATE: 12/11/2011

TIME: 13:04:52

Input Set : A:\ES.txt

Output Set : N:\CRF3\12112001\I002292.raw

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69 <211> LENGTH: 35
70 <212> TYPE: DNA
71 <213> ORGANISM: Lambda phage
73 <220> FEATURE:
74 <221> NAME/KEY: misc_feature
75 <222> LOCATION: (1)..(35)
76 <223> OTHER INFORMATION: Primer for Polymerase Chain Reaction (PCR)
79 <400> SEQUENCE: 4
80 ggaactctatg aggtatctga aatcagccac aagcgc 35
83 <210> SEQ ID NO: 5
84 <211> LENGTH: 23
85 <212> TYPE: DNA
86 <213> ORGANISM: Lambda phage
88 <220> FEATURE:
89 <221> NAME/KEY: misc_feature
90 <222> LOCATION: (1)..(23)
91 <223> OTHER INFORMATION: Primer for Polymerase Chain Reaction (PCR)
94 <400> SEQUENCE: 5
95 cagtcacgac attgtaaaac gac 23
98 <210> SEQ ID NO: 6
99 <211> LENGTH: 23
100 <212> TYPE: DNA
101 <213> ORGANISM: Lambda phage
103 <220> FEATURE:
104 <221> NAME/KEY: misc_feature
105 <222> LOCATION: (1)..(23)
106 <223> OTHER INFORMATION: Primer for Polymerase Chain Reaction (PCR)
109 <400> SEQUENCE: 6
110 cacaggaac agctatgacc atg 23
113 <210> SEQ ID NO: 7
114 <211> LENGTH: 23
115 <212> TYPE: DNA
116 <213> ORGANISM: Lambda phage
118 <220> FEATURE:
119 <221> NAME/KEY: misc_feature
120 <222> LOCATION: (1)..(23)
121 <223> OTHER INFORMATION: Primer for Polymerase Chain Reaction (PCR)
124 <400> SEQUENCE: 7
125 ggaatcagt tcattttcq tca 23
128 <210> SEQ ID NO: 8
129 <211> LENGTH: 22
130 <212> TYPE: DNA
131 <213> ORGANISM: Lambda phage
133 <220> FEATURE:
134 <221> NAME/KEY: misc_feature
135 <222> LOCATION: (1)..(22)
136 <223> OTHER INFORMATION: Primer for Polymerase Chain Reaction (PCR)
139 <400> SEQUENCE: 8
140 gtatggcagc cgaatgaca ga 22

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RAW SEQUENCE LISTING

PATENT APPLICATION NO: US/10/002,292

DATE: 12/11/2001

TIME: 11:41:32

Input Seq : A:\ES.txt

Output Seq : N:\CRF3\12112001\I002292.raw

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143 <210> SEQ ID NO: 9
144 <211> LENGTH: 558
145 <212> TYPE: DNA
146 <213> ORGANISM: Escherichia coli
148 <400> SEQUENCE: 9
149 agcttctcga gattccctatt ctggaaaacc gggctgctca gggcgatatt actgcacccg      60
151 ggggtgctcg ccgttttaacg ggtgatcaga ctgccctctt gctgattctt cttagcgata      120
153 aacctgaaaa aaatattatt ttgctgattt gggatgggat gggggactcg gaaattactg      180
155 cggacacgtaa ttatgcgaaa ggtgcggggc gcttttttaa aggtatagat gcttaccgcg      240
157 ttaccgggca atacactcac tatgcctcga ataaaaaaaa cggcaaacgc gactacgtca      300
159 cggactcggc tgcatacaga accgcctggg caaccgggtg caaaccttat aacggcgcgcg      360
161 tggcgctcga tatcacgaa aaagatcac caacgattct ggaatatgca aaagcgcgag      420
163 gctcgcgac cggtaacgtt tctaccgcag agttgcagga tggcacgccg gctgcgctgg      480
165 tggcacatgt gacctcgcgc aaatgctacg gtccgagcgc gaccagtga aaatgtccgg      540
167 gtaacgctct ggaaaaag
170 <210> SEQ ID NO: 10
171 <211> LENGTH: 8
172 <212> TYPE: PRT
173 <213> ORGANISM: Artificial Sequence
175 <220> FEATURE
176 <221> NAME/KEY: BINDING
177 <222> LOCATION: (1)..(8)
178 <223> OTHER INFORMATION: TAG USED TO PURIFY RECOMBINANT PROTEIN
181 <400> SEQUENCE: 10
183 Asp Tyr Lys Asp Asp Asp Asp Lys
184 1 5
186 <210> SEQ ID NO: 11
187 <211> LENGTH: 63
188 <212> TYPE: DNA
189 <213> ORGANISM: Artificial Sequence
191 <220> FEATURE
192 <221> NAME/KEY: promoter
193 <222> LOCATION: (1)..(63)
W--> 195 <223> OTHER INFORMATION:
195 <400> SEQUENCE: 11
196 ggaatcctaat acgactcact atagggaqaa gggccaccat ggactacaaa gacgatgacg      60
198 aca
201 <210> SEQ ID NO: 12
202 <211> LENGTH: 63
203 <212> TYPE: DNA
204 <213> ORGANISM: Artificial Sequence
206 <220> FEATURE
207 <221> NAME/KEY: promoter
208 <222> LOCATION: (1)..(63)
W--> 210 <223> OTHER INFORMATION:
210 <400> SEQUENCE: 12
211 cctacgattt tactgaattg tatccctctt cccggtggtt cctgatgttt ctactactgc      60
213 tgt
216 <210> SEQ ID NO: 13

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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/002,292

DATE: 12/11/2001

TIME: 12:04:30

Input Set: A:\ES.txt

Output Set: N:\CRF3\12112001\I002292.raw

217 <211> LENGTH: 37

218 <212> TYPE: RNA

219 <213> ORGANISM: Artificial Sequence

221 <220> FEATURE:

222 <221> NAME/KEY: primer_bind

223 <222> LOCATION: (1)..(50)

W--> 225 <223> OTHER INFORMATION: /

225 <400> SEQUENCE: 13

226 gatctttgaaa actaaccata cgtcatgtgc ccaccagcct tgtccataata

50

229 <210> SEQ ID NO: 14

230 <211> LENGTH: 46

231 <212> TYPE: DNA

232 <213> ORGANISM: Artificial Sequence

234 <220> FEATURE:

235 <221> NAME/KEY: primer_bind

236 <222> LOCATION: (1)..(46)

W--> 238 <223> OTHER INFORMATION: /

238 <400> SEQUENCE: 14

239 aactttttgat tggatatgcaq tacacgggtg qtcqqaacag gatttat

46

VERIFICATION SUMMARY

PATENT APPLICATION No: US/10/002,292

DATE: 12/11/2001

TIME: 12:04:33

Input Set : A:\ES.txt

Output Set : N:\CRF3\12112001\I002292.raw

L:19 M:271 W: Current Application Number differs. Replaced Current Application No.

L:19 M:271 W: Current Filing Date differs. Replaced Current Filing Date

L:195 M:258 W: Mandatory Feature missing. <223> OTHER INFORMATION:

L:216 M:258 W: Mandatory Feature missing. <223> OTHER INFORMATION:

L:225 M:258 W: Mandatory Feature missing. <223> OTHER INFORMATION:

L:238 M:258 W: Mandatory Feature missing. <223> OTHER INFORMATION: